SEQUENCE LISTING

<110> KOJIMA, SHIN-ICHI
ASAKURA, AKIRA
FUTATSUGI, TETSUAKI
OTA, YUKO
FUKUDA, YUKI
SAGARA, SHINSUKE

<120> NOVEL INTERFERON-ALPHA

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<140> 09/889,035
<141> 2001-07-11

<150> JP 11-5138
<151> 1999-01-12

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<212> DNA
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<400> 1

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Met Ala Leu Ser Phe Ser Leu Leu Met Ala Val Leu Val Leu Ser Tyr
                  5                  10                  15

aaa tcc atc tgt tct cta ggc tgt gat ctg cct cag acc cac agc ctg      96
Lys Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
             20                  25                  30

ggt aat agg agg gcc ttg ata ctc ctg gca caa atg gga aga atc tct     144
Gly Asn Arg Arg Ala Leu Ile Leu Leu Ala Gln Met Gly Arg Ile Ser
         35                  40                  45

cct ttc tcc tgc ctg aag gac aga cat gat ttc cga atc ccc cag gag     192
Pro Phe Ser Cys Leu Lys Asp Arg His Asp Phe Arg Ile Pro Gln Glu
     50                  55                  60

gag ttt gat ggc aac cag ttc cag aag gct caa gcc atc tct gtc ctc     240
Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Gln Ala Ile Ser Val Leu
 65                  70                  75                  80

cat gag atg atc cag cag acc ttc aat ctc ttc agc aca gag gac tca     288
His Glu Met Ile Gln Gln Thr Phe Asn Leu Phe Ser Thr Glu Asp Ser
                 85                  90                  95

tct gct gct tgg gaa cag agc ctc cta gaa aaa ttt tcc act gaa ctt     336
Ser Ala Ala Trp Glu Gln Ser Leu Leu Glu Lys Phe Ser Thr Glu Leu
            100                 105                 110
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tac cag caa ctg aat gac ctg gaa gca tgt gtg ata cag gag gtt ggg      384
Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Glu Val Gly
        115                 120                 125

gtg gaa gag act ccc ctg atg aat gag gac tcc atc ctg gct gtg agg      432
Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Ile Leu Ala Val Arg
    130                 135                 140

aaa tac ttc caa aga atc act ctt tat cta ata gag agg aaa tac agc      480
Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Ile Glu Arg Lys Tyr Ser
145                 150                 155                 160

cct tgt gcc tgg gag gtt gtc aga gca gaa atc atg aga tcc ctc tcg      528
Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Leu Ser
                165                 170                 175

ttt tca aca aac ttg caa aaa aga tta agg agg aag gat                  567
Phe Ser Thr Asn Leu Gln Lys Arg Leu Arg Arg Lys Asp
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac       96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
            20                  25                  30

aga cat gat ttc cga atc ccc cag gag gag ttt gat ggc aac cag ttc      144
Arg His Asp Phe Arg Ile Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
        35                  40                  45

cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc      192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
    50                  55                  60

ttc aat ctc ttc agc aca gag gac tca tct gct gct tgg gaa cag agc      240
Phe Asn Leu Phe Ser Thr Glu Asp Ser Ser Ala Ala Trp Glu Gln Ser
65                  70                  75                  80

ctc cta gaa aaa ttt tcc act gaa ctt tac cag caa ctg aat gac ctg      288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
                85                  90                  95

gaa gca tgt gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg      336
Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
            100                 105                 110

aat gag gac tcc atc ctg gct gtg agg aaa tac ttc caa aga atc act      384
Asn Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
        115                 120                 125
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ctt tat cta ata gag agg aaa tac agc cct tgt gcc tgg gag gtt gtc      432
Leu Tyr Leu Ile Glu Arg Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
    130                 135                 140

aga gca gaa atc atg aga tcc ctc tcg ttt tca aca aac ttg caa aaa      480
Arg Ala Glu Ile Met Arg Ser Leu Ser Phe Ser Thr Asn Leu Gln Lys
145                 150                 155                 160

aga tta agg agg aag gat                                             498
Arg Leu Arg Arg Lys Asp
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Gly Asn Arg Arg Ala Leu Ile Leu Leu Ala Gln Met Gly Arg Ile Ser
         35                  40                  45

Pro Phe Ser Cys Leu Lys Asp Arg His Asp Phe Arg Ile Pro Gln Glu
     50                  55                  60

Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Gln Ala Ile Ser Val Leu
 65                  70                  75                  80

His Glu Met Ile Gln Gln Thr Phe Asn Leu Phe Ser Thr Glu Asp Ser
                 85                  90                  95

Ser Ala Ala Trp Glu Gln Ser Leu Leu Glu Lys Phe Ser Thr Glu Leu
            100                 105                 110

Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Glu Val Gly
        115                 120                 125

Val Glu Glu Thr Pro Leu Met Asn Glu Asp Ser Ile Leu Ala Val Arg
    130                 135                 140

Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Ile Glu Arg Lys Tyr Ser
145                 150                 155                 160

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Leu Ser
                165                 170                 175

Phe Ser Thr Asn Leu Gln Lys Arg Leu Arg Arg Lys Asp
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Arg His Asp Phe Arg Ile Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Glu Asp Ser Ser Ala Ala Trp Glu Gln Ser
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Ile Glu Arg Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Leu Ser Phe Ser Thr Asn Leu Gln Lys
145 150 155 160

Arg Leu Arg Arg Lys Asp
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5 10 15

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20 25 30

Arg His Asp Phe Xaa Ile Pro Gln
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<210> 6
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<400> 6
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<210> 7
<211> 34
<212> DNA
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<400> 7
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